

BLAST

Basic Local Alignment Search Tool

[NCBI BLAST/blast.cgi/](#) [Format Results - NXBHZ2601N](#)

gb|AF172172.1| (483 letters)

Query ID [gb|AF172172.1|](#)
Description Medicago sativa non-symbiotic hemoglobin (MHB1) mRNA, complete cds
Molecule type nucleic acid
Query Length 483

Database Name nr
Description All GenBank+ EMBL+ DDBJ+ PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
Program BLASTN 2.2.25+

Descriptions

 Legend for links to other resources: [UniGene](#) [GEO](#) [Gene](#) [Structure](#) [Map Viewer](#) [PubChem BioAssay](#)

Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
AF172172.1	Medicago sativa non-symbiotic hemoglobin (MHB1) mRNA, complete cds	693	693	100%	0.0	100%	
BJ068828.1	Soybean clone JCVI-FLGM-10A5 unknown mRNA	571	571	94%	1e-159	89%	U
AB233220.1	Lotus japonicus LjHb1 mRNA for nonsymbiotic hemoglobin, complete cds	527	527	95%	3e-146	87%	U
AY066062.1	Gossypium hirsutum non-symbiotic hemoglobin protein mRNA, complete cds	442	442	88%	1e-120	85%	U
AF322348.1	Gossypium hirsutum non-symbiotic hemoglobin class 1 (GLB1) mRNA, complete cds	427	427	88%	3e-116	84%	U
AB221244.1	Alnus firma mRNA for nonsymbiotic hemoglobin, complete cds	390	390	95%	4e-105	81%	
AY224133.1	Pyrus communis non-symbiotic hemoglobin class 1 (GLB1) mRNA, complete cds	368	368	96%	2e-98	81%	
G042618.1	Malus hupehensis non-symbiotic hemoglobin mRNA, complete cds	340	340	96%	4e-90	80%	
AY208331.1	Raphanus sativus nonsymbiotic hemoglobin mRNA, complete cds	244	244	93%	3e-61	77%	U
J01133.1	Glycine max nonsymbiotic hemoglobin gene, complete cds	206	206	27%	1e-49	94%	E
XM_002272282.1	PREDICTED: Vitis vinifera hypothetical protein LOC100253215 (LOC100253215), mRNA	176	176	33%	1e-40	86%	GM
Y06986.1	Trema tomentosa haemoglobin gene	167	167	28%	7e-38	88%	
AP019323.1	Lotus japonicus genomic DNA, chromosome 3, clone: LJ27C23, TM0091, complete sequence	163	163	23%	9e-37	92%	
AP004623.1	Lotus japonicus genomic DNA, chromosome 3, clone: LJ20701, TM0091a, complete sequence	163	163	23%	9e-37	92%	
Z09355.1	Trema orientalis hemoglobin gene	158	158	28%	4e-35	87%	
AF327218.1	Trema orientalis hemoglobin gene, complete cds	153	158	28%	4e-35	87%	
A113135.1	Trema virgata gene encoding hemoglobin, isolate T4	145	145	28%	3e-31	85%	
A113130.1	Trema virgata gene encoding hemoglobin, isolate T2	145	145	28%	3e-31	85%	
A113149.1	Trema virgata gene encoding hemoglobin, isolate T1	145	145	28%	3e-31	85%	

NOP

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Alignments

>gb|AF172172.1|AF172172 Medicago sativa non-symbiotic hemoglobin (MHB1) mRNA, complete cds
Length=483

Score = 893 bits (483), Expect = 0.0
Identities = 483/483 (100%), Gaps = 0/483 (0%)
Strand=Plus/Plus

```
Query 1 ATGGGACCTTTGGATACAAAGGTTTCACTGGAAGAACAAAGCTCTTGGTGAAGTCA 60
Sbjct 1 ATGGGACCTTTGGATACAAAGGTTTCACTGGAAGAACAAAGCTCTTGGTGAAGTCA 60
Query 61 TGGAAATGCAATGAAGAAATTTCTGCAGAGTTAGGACTAAAGCTTTTCTGAAATATTT 120
Sbjct 61 TGGAAATGCAATGAAGAAATTTCTGCAGAGTTAGGACTAAAGCTTTTCTGAAATATTT 120
Query 121 GAGATTGCTCCATCAGCTGAAAACTTTTCTCATTCTTGAAGATTCAAAATGCTTTG 180
Sbjct 121 GAGATTGCTCCATCAGCTGAAAACTTTTCTCATTCTTGAAGATTCAAAATGCTTTG 180
Query 181 GAGCAAAACACCAAGCTCAAGGCTCATGCCATGTCGTCTTCTCATGACATGTGAATCA 240
Sbjct 181 GAGCAAAACACCAAGCTCAAGGCTCATGCCATGTCGTCTTCTCATGACATGTGAATCA 240
Query 241 GCGGTTCAACTGCGGAAATCCGGTAAAGTTACGGTCAGAGAAATCAAGCTTGAAAAATTA 300
Sbjct 241 GCGGTTCAACTGCGGAAATCCGGTAAAGTTACGGTCAGAGAAATCAAGCTTGAAAAATTA 300
Query 301 GGTGCTAACCATTTTAAATACGGTGTAGTAGACGAGCATTTTGAGGTGACAAAGTTTGA 360
Sbjct 301 GGTGCTAACCATTTTAAATACGGTGTAGTAGACGAGCATTTTGAGGTGACAAAGTTTGA 360
Query 361 CTTTGGAGACCATATAAAGAAAGCAGTACCTGAAATGTGGTACCGGCTATGAAGAAATGA 420
Sbjct 361 CTTTGGAGACCATATAAAGAAAGCAGTACCTGAAATGTGGTACCGGCTATGAAGAAATGA 420
Query 421 TGGGGAGAAGCTTATGATCAGTTGGTCAATGCAATCAAATCTGAATGAAACCTTCTCT 480
Sbjct 421 TGGGGAGAAGCTTATGATCAGTTGGTCAATGCAATCAAATCTGAATGAAACCTTCTCT 480
Query 481 TAG 483
Sbjct 481 TAG 483
```

>gb|BT096529.1| Soybean clone JCVI-FLGm-10A5 unknown mRNA
Length=751

Score = 571 bits (309), Expect = 1e-159
Identities = 462/461 (99%), Gaps = 9/461 (1%)
Strand=Plus/Plus

```
Query 18 AAA-AGGTTTCACTGAAAGAACAAAGAGCTCTTGGTGAAGTCAAGAAATG-CAATGAAG 75
Sbjct 102 AAAGAGGTTTCTCGGAGAGCAAGAGAGCTCTGGTGGTGAAGTCAAGAAATGTC-ATGAG 160
Query 76 AAGAATTCTGCAGAGTTAGGACTAAAGCTTTTCTGAAAAATATTGAGATTGCTCCATCA 135
Sbjct 161 AAGAATTCTGGAAGAGTTGGGTCTCAAGTTTCTTGAATAATATTGAGATTGCTCCATCA 220
Query 136 GCTCAAAAACCT-TTCTCATTCTTGAAGAGTCAAAAAGTTCTCTTGGAGCAAAA-CACCA 193
Sbjct 121 GCTCAGAAA-TTGTCTCATTCTTGGAGAGATCAACGGTCTCTTGGAGCAAAA-CGA 278
Query 194 AGCTCAAGGCTCATGCCATGTCGTCTTCTCATGACATGTGAATCAGCGGTCACATGCG 253
Sbjct 279 AGCTCAAGGCTCATGCCATGTCGTCTTCTCATGACATGTGAATCAGCGGTCACATGCG 338
Query 254 GAAATCCGGTAAAGTTACGGTCAGAGAAATCAAGCTTGAAAAAATTAGGTGCTAACCAT 313
Sbjct 339 GAAAGGCGGGAAAGTCACTGTCAGAGAAATCAAACTTGAAAAAATTAGGTGCTAACCAT 398
Query 314 TTA-AATACGGTGTAGTAGACGAGCATTTTGAGGTGACAAAGTTTGACATTTTGGAGACC 372
Sbjct 399 TTAGAA-CCGGGCTAGCAACGAGCATTTCGAGGTGACAAAGTTTGACATTTTGGAGACC 457
Query 373 ATAAAAAGAGCAGTACCTGAAATGTGGTACCGGCTATGAAGAAATGATGGGGAAGAGCT 432
Sbjct 458 ATAAAAAGAGCAGTACCTGAAATGTGGTACCGGCTATGAAGAAATGATGGGGAAGAGCT 517
Query 433 TATGATCAGTTGGTCAATGCAATCAAATCTGAAATGAAACC 473
Sbjct 518 TATGATCAGTTGGTCAATGCAATCAAATCTGAAATGAAACC 558
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>dbj|AB238220.1| Lotus japonicus LjHb1 mRNA for nonsymbiotic hemoglobin, complete cds
Length=486

Score = 527 bits (285), Expect = 3e-146
Identities = 402/460 (88%), Gaps = 2/460 (0%)
Strand=Plus/Plus

```
Query 23 GTTTCACCTGAAGAACAAAGAGCTCTTGGTGGTGAAGTCATGGAATGCAATGAAGAAGATT 82
Sbjct 23 GTTTCACCTGAAGAGCAAGAGCTCTTGGTGGTGAAGTCATGGAAGGTGATGAAGAAGATT 82
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Query 83  CTGCAGAGTTAGGACTAAAGCTTTTCTTGAAAAATATTTGAGATTGCTCCATCAGCTCAAA 142
Sbjct 83  CTGCTGAAGCTGGGCTCAAGCTTTTCTTGAAAAATATTTGAGATTGCTCCATCAGCTCAAG 142
Query 143  AACTT-TTCTCATCTCTTGAAGATTCAAAAGTTCTCTTTGGAGCAAAACACCAAGCTCAAG 201
Sbjct 143  AA-TTGTCTCTCTTCTTGAGAGATTCAAAAGTTCTCTTTGGAGGAGAACCCCAAGCTCAAG 201
Query 202  CCTCATGCCATGTCTGTCTTTCTCATGACATGTGAATCAGCGGTTCACATGGCGAAATCC 261
Sbjct 202  CCTCATGCCATGTCTGTCTTTCTCATGACATGTGAATCAGCGGTTCACATGGCGAAGGT 261
Query 262  GGTAAAGTTACGCTCAGAGAACTAAAGCTTGAAAAATATAGGTGCTAACCATTTTAAATAC 321
Sbjct 262  GGAAGAACTCACTGTGAGAGAACTAACCTTGAAAAAGCTAGGTGCTAACCATTTAATAT 321
Query 322  GGTGTAGTAGACAGCAATTTTGAAGTGAACAGTTTGACATTTTGAGAGCAATAAAAGAA 381
Sbjct 322  GAGTAGTAAACGAGCAATTTTGAAGTGAACAGTTTGACATTTTGAGTACCAATAAAAGAA 381
Query 382  CAGCTACCTGAAATGTGGTCAACCGCTATGAAGAATGCATGGGAGAAAGCTTATGATCAG 441
Sbjct 382  GCTGTACCTGAAATGTGGTCAACCGAGATGAAGAATGCATGGGAGAAAGCTTATGATCAG 441
Query 442  TTGGTCAATGCAATCAAACTGAAATGAAGAACTTCTCTTT 481
Sbjct 442  CTGGTCGGTGCAATTAATCTGAAATGAAGCAATCATCTT 481


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>gb|AY899302.1|  Gossypium hirsutum non-symbiotic hemoglobin protein mRNA, complete cds
Length=813

```

Score = 442 bits (239), Expect = 1e-120
Identities = 370/433 (86%), Gaps = 10/433 (2%)
Strand=Plus/Plus
Query 19  AAAGGTTTCACTGAAGAAACAAAGAGCTCTT-TGTTGGAAGTCATGGAATGCAATGAAGAA 77
Sbjct 69  AAAGTTTCACTGAAGAAACAAAGAGCT-TTGGTGGTCAAGTCATGAGCTTAATGAAGAA 127
Query 78  GAATTCGAGAGTTAGAAC-TAAAGCTT-TTCTTGAAAAATATTTGAGATTGCTCCATCA 135
Sbjct 128  GAATGCAGCTGAATTTGGGTCTTAAA---TTCTTCTTGAGAGATTTGAGATTGCAACATCA 185
Query 136  GCTCAA-AACTTTTCTCATCTTGAAGAGATCAAAAGTTCTCTTTGGAGCAAAACACCAA 194
Sbjct 186  GC-CAAGAAACTATTCTCATCTTGAGAGACTCCAAATGTTCCATTGGAGCAAAACACCAA 244
Query 195  GCTCAAGCCTCATGCCATGTCTGTCTTTCTCATGACATGTGAATCAGCGGTTCACATGGG 254
Sbjct 245  GCTGAAGCCCATGCCATGTCTGTCTTTGTCATGACATGTGAATCAGAGTTTCACTGGG 304
Query 255  GAAATCCGTTAAAGTTACGCTCAGAGAACTCAAGCTTGAAAAATATAGGTGCTAACCATTT 314
Sbjct 305  TAAAGCAGGCAAGATTACAGTGAAGGAACTCAAAATTTGAAGAAATAGGAGCTACCATTT 364
Query 315  TAAATACGGTGTAGTAGACAGCAATTTTGAAGTGACAAAGTTTGACATTTTGAAGACCAT 374
Sbjct 365  TAAGTATGGGTAGTTGATGAACATTTTGAGGTAAACAAATTTGCTCTTTTGAGAGCAAT 424
Query 375  AAAAGAAGCAGTACCTGAAATGTGGTCAACCGCTATGAAGAATGCATGGGAGAAAGCTTA 434
Sbjct 425  AAAAGAAGCAGTACCAAGATATGTGGTCAGATGAGATGAAGAAATGCATGGGAGAGCCTA 484
Query 435  TGATCAGTT-GGT 446
Sbjct 485  TGATC-GTTTGGT 496

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>gb|AF329368.1|AF329368  Gossypium hirsutum non-symbiotic hemoglobin class 1 (GLB1) mRNA, complete cds
Length=634

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Score = 427 bits (231), Expect = 3e-116
Identities = 368/434 (85%), Gaps = 10/434 (2%)
Strand=Plus/Plus
Query 19  AAAGGTTTCACTGAAGAAACAAAGAGCTCTT-TGTTGGAAGTCATGGAATGCAATGAAGAA 77
Sbjct 37  AAAGTTTCACTGAAGAAACAAAGAGCT-TTGGTGGTCAAGTCATGAGCTTAATGAAGAA 95
Query 78  GAATTCGAGAGTTAGAAC-TAAAGCTT-TTCTTGAAAAATATTTGAGATTGCTCCATCA 135
Sbjct 96  GAAACAGCTGAATTTGGGTCTTAAA---TTCTTCTTGAGAGATTTGAGATTGCAACATCA 153
Query 136  GCTCAA-AACTTTTCTCATCTTGAAGAGATCAAAAGTTCTCTTTGGAGCAAAACACCAA 194
Sbjct 154  GC-CAAGAAACTATTCTCATCTTGAGAGACTCCAAATGTTCCATTGGAGCAAAACACCAA 212
Query 195  GCTCAAGCCTCATGCCATGTCTGTCTTTCTCATGACATGTGAATCAGCGGTTCACATGGG 254
Sbjct 213  GCTGAAGCCCATGCCATGTCTGTCTTTGTCATGACATGTGAATCAGAGTTTCACTGGG 272
Query 255  GAAATCCGTTAAAGTTACGCTCAGAGAACTCAAGCTTGAAAAATATAGGTGCTAACCATTT 314

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Sbjct 273 TAAAGCAGGCAAGTTACAGTGAGGGAATCAAAATTTGAAGAAATAGGAGCTACCCATT 332
Query 315 TAAATACGGTGTAGTAGACGAGCATTTTGAAGGTGACAAAGTTTGCACCTTTTGAGACCAT 374
Sbjct 333 TAAGTATGGGTAGTTGATGAACATTTTGAAGTAAACAAATTTGCTCTTTTGAGACCAT 392
Query 375 AAAAGAGCAGTACCTGAAATGTGGTCACGGCTATGAAGAAATGCATGGGAGAGCTTA 434
Sbjct 393 AAAAGAGCAGTACAGGATATGTGGTCAGATGAGATGAAGAAATGCATGGGAGAGCTTA 452
Query 435 TGATCAGTT-GGTC 447
Sbjct 453 TGATC-GTTGGTC 465

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>dbj|AB221344.1| *Alnus firma* mRNA for nonsymbiotic hemoglobin, complete cds
length=483

Score = 390 bits (211), Expect = 4e-105
Identities = 382/466 (82%), Gaps = 6/466 (1%)
Strand=Plus/Plus

```

Query 21 AGGTTTCACTGAAGAACCAAGAGCTCTTGTGGTGAAGTCATGGAATGCAATGAAGAAGAA 80
Sbjct 21 AGGGTTCCAGAGAAAGCAAGAGCTGTGGTGGTGAAGTCATGGAATGCAATGAAGCCATA 80
Query 81 TTCTGCAGAGTTAGGACTAAAGCTT-TTCTTGAATAATTTGAGATTGCTCCATCAGCTC 139
Sbjct 81 TGCTGGAGAAATGGGTCTAAA-ATTCTCTTGAAGATATTGAGATTGCACCATCAGCTC 139
Query 140 AAAAACCTTTCTCATCTCTTGAAGATTCAAAAGTTCTCTTTGGAGC-AAACACCAAGAGCT 198
Sbjct 140 AGAAGCTCTCTCTTCTTCTTGAAGAGACTCAAAATGTTCTCTCGAAGAAATC-CAAGGCT 198
Query 199 AAG-CCATGCGCATGTCTGTCTTTCTCATGACATGTGAATCAGCGCTTCAACTGCGGAA 257
Sbjct 199 AAGTCC-CATGCGCATGTCTGTCTCTCATGACCTGTGAATCGGCAAGTGCACCTCGGAA 257
Query 258 ATCCGGTAAAGTTACGGTCAGAGAAACAAGCTTGAAGAAATAGGTGCTAACCAATTTAA 317
Sbjct 258 AGCCGGCAAGATTACTGTGAGAGAGTCGAGCTTGAAGAAATGGGTGCTTCCACTTCAA 317
Query 318 ATCAGGTGTAGTAGACGAGCATTTTGAAGTGAACAAAGTTTGCACCTTTTGAAGACCATAA 377
Sbjct 318 GCATGGGGTGGTGCATGAACATTATGAGGTACAAAGTTTGCCTGCTGGAAGACTTCAA 377
Query 378 AGAAGCAGTACCTGAJAATGTGGTCACCGGCTATGAAGAAATGCATGGGAGAGAGCTTATGA 437
Sbjct 378 GGAAGCGGTGCCAGAAATGTGGTCACCGGAGATGAAGATTGCATGGGAGAGAGCTTATGA 437
Query 438 TCAGTTGGTCAATGCAATCAAAATCTGAAATGAACCTTCTCTTAG 483
Sbjct 438 TCAGTTGGTGTGCTATCAAAATCTGCAATGAAGGCTTCTCTTAG 483

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>gb|AY224133.1| *Pyrus communis* non-symbiotic hemoglobin class 1 (GLB1) mRNA,
complete cds
length=477

Score = 368 bits (199), Expect = 2e-98
Identities = 385/473 (82%), Gaps = 19/473 (4%)
Strand=Plus/Plus

```

Query 19 AAGGTTTCACTGAAGAACCAAGAGCTCTTGTGGTGAAGTCATGGAATGCAATGAAGAAG 78
Sbjct 10 AAGGTTTCCAGAGAAAGCAGGAAACACTGGTGGTGAAGTCATGGGGTGTGATGAAGCAG 69
Query 79 AATCTGCAGAGTTAGGACTAAAGCTT-TTCTTGAATAATTTGAGATTGCTCCATCAGC 137
Sbjct 70 AATGCTGCTGATTGGGGCTTAAAG-TTCTCTTGAAGATCTTGAATGTCACCATCAGC 128
Query 138 TCAAAAACTTTTCTCATCTTGAAGATTC-AAAAGTTCTCT-TTGGAGCAA-AAACCC-A 193
Sbjct 129 TCAGAACTGTCTCTCTTCTTGAAGGACTCTAATA-TTCTCTT-GAG-AAAGAA-CCAA 184
Query 194 AGCTCAAGGCTCATGCGATGTCTGTCTTTCTCATGACATGTGAATCAGCGGTCAAGTCG 253
Sbjct 185 AGCTCAAGGCTCATGCGATGTCTGTATTGTTATGACTTGTGAATCAGCAGTTCAACTC 243
Query 254 -GGAAATCCGGTAAAGTTACGGTCAGAGAAACAAGCTTGAAGAAATAGGTGCTAACCAT 312
Sbjct 244 AGGAAAGCAGGCAAGGTTACAGTGAGAGAGTCAACCTTGAAGAAATAGGTGGTGTCCAC 303
Query 313 TTTAAATAC-GGTGTAGTAGACGAGCATTTTGAAGTGAACAAAGTTTGCACCTT-TTGAGA 370
Sbjct 304 TTCAAGT-CTGGAGTGGTAGATGAACATTATGAGGTGACCAAGTGTGCA-TTGTGGAAA 361
Query 371 CCATTAAGAGAGCAGTACCTGAAATGTGGTCACCGGCTATGAAGAAATGCATGGGAGAG 430
Sbjct 362 CCATTAAGAGAGCCGTACCCGAAATGTGGTCACCGGAGATGAAGAAATGCATGGGAGAG 421
Query 431 CTTATGATCAGTTGGTCAATGCAATCAAAATCT-GAAATGAACCTTCTCTTAA 482
Sbjct 422 CTTATGATCAGTTGGTTACTGCTATAAAAT-TAGAAATGAAGGCTCTCC-CTTA 472

```

>gb|GQ423619.1| *Malus hupehensis* non-symbiotic hemoglobin mRNA, complete cds
length=477

Score = 340 bits (184), Expect = 4e-90
 Identities = 380/473 (81%), Gaps = 19/473 (4%)
 Strand=Plus/Plus

```

Query 19  AAAGGTTTCACTGAAGAACAAAGAGCTCTTGTGGTGAAGTCATGGAATGCAATGAAGAAG 78
Sbjct 10  AAAGTTTTCACAGAGAAGACAGGAAACACTGGTGGTGAAGTCATGGGGTGTGATGAAGAAG 69

Query 79  AATCTGACAGAGTAGCACTAAAGCTT-TTCTTGAAA-ATATTTGAGATTGCTCCATCAG 136
Sbjct 70  AAGCTGCTGAATTGGGCTTTAAG-TTCTCTT-AAAGACTTTTGAATGACACATGAG 127

Query 137  CTCAAAAACCTTTTCTCATCTTGAAGAGTTC-AAAAGTTCTCT-TTGAGCAA-AACACC- 192
Sbjct 128  CTCAGAAAGCTGTCTCTTTCTTGAGGGACTCTGACA-TTCTCTT-GAG-AAGAAC-CCA 183

Query 193  AAGCTCAAGCCTCATGCGATGCTGTCTTCTCATGACATGGAATCAGCCCTCAACTG 252
Sbjct 184  AAGCTCAAGCCTCAGCCATGTCTGATTAGTTATGATCTTGAATCAGCACTCAACT 242

Query 253  C-GGAATCCGGTAAAGATTACGCTCAGAGAATCAAGCTTGAAAATAATTAGTGCTTACCA 311
Sbjct 243  CAGGAAAGCAGGCAAGGTTACAGTGAGAGAGTCAACCTTGAAAAGATTAGTGCTTCCA 302

Query 313  TTTTAAATAC-GGTGTAGTAGACGAGCACTTTGAGGTGACAAAGTTTGCACTT-TTGGAG 369
Sbjct 303  CTTCAGT-CTGGAGTGGTAGATGAACATTATGAGGTGACCAAGTTGCA-TTGTGGAA 360

Query 370  ACCATAAAGAGAACGACTACCTGAAATGTGGTCAACCGGCTATGAAGAATGCATGGGAGAA 429
Sbjct 361  ACCATAAAGAGGCTCTACCGGAAATGTGGTCAACCGGAGATGAAGAATGCATGGGAGAA 420

Query 430  GCTTATGATCATGTGGTCAATGCAATCAAACTGAAAATGAAACCTTCTCTTA 482
Sbjct 421  GCTTATGATCAGTTGGTTGCTGCTATAAAATCAGAAATGAAGCTCCCTCCTTA 472

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>gb|AY286331.1| *Raphanus sativus* nonsymbiotic hemoglobin mRNA, complete cds
 Length=683

Score = 244 bits (132), Expect = 3e-61
 Identities = 359/466 (77%), Gaps = 25/466 (5%)
 Strand=Plus/Plus

```

Query 23  GTTTCACCTGAAGAACAAAGAGCTCTTGTGGTGAAGTCATGGAATG-CAATGAAGAAGAAT 81
Sbjct 74  GTTT-ACAGAGAGACAAAGAGCTCTTGTGGTGAAGTCATGGAATGTCA-TGAAGAAAATAT 131

Query 82  TCTGCAGAGTTAGGACT-AAAGCTTTTCTTGAAAATATTGAGATTGCTCCATCAGCTCA 140
Sbjct 132  TCAGCTGATTTGGGTCTCAAA-CTATTTCATCAAGATCTTTGAGATTGACCAACAGGG-A 189

Query 141  AAAACCTT-TTCTCATCTTTGAAAGATTCAAA-AGTTCTCTT-TGGAGCAAAACCAACAA-GC 196
Sbjct 190  AGAAGTTGTCTGTGTTTTGAGAGACTCACCCA-TCCCTGCTG-AGCAAAAC-CAAGAGC 246

Query 197  TCAAGCCTCATGCGCATGCTGTCTTTTCTCATGACATGGAATCAGCGCTTCAACTGGGGA 256
Sbjct 247  TCAAGCCTCATGCCATGCTGTGTTTTTTCATGTGTGTGAGTCAAGCAGCAGCTGAGAA 306

Query 257  AATCCGGTAAAGTTACGGTCA-G-AGAATCAAGCTTGAAAAAATTAGTGCTAACCACTT 314
Sbjct 307  AAGACGGAAGAAATTTACAGTGAAGGAGA--CAACCTGAGAGGCTAGAGCCAACTATCT 364

Query 315  TAAATACGGGTGTAGTAGACAGCACTTTTGGAGTGACAAAGTTTGCACTT-TTGAGACCA 373
Sbjct 365  TAAATACGGGCTGTGTGATGAACACTTTTGGAGTGACCAAGTATGCA-TTGTGTGGAGACA 423

Query 374  TAAAGAGAGCAGTACCTGAAATGTGGTCAACCGGCTATGAAGAA-TGCATGGGAGAGCT 432
Sbjct 424  TAAAGAGGCGGTGTGCGGAGATGTGGTCAACCGGAAATGAA-ATCTGCTGGGGTCAGGCT 482

Query 433  TATGATCAG-TTGGT-CAATGCAATCAAACTGAAATGAAACCTTC 476
Sbjct 483  TATGATCACCTTGTGTG--TGCCATTAAAGCTGAAATGAAGCTTC 526

```

>gb|U47143.1| *Glycine max* nonsymbiotic hemoglobin gene, complete cds
 Length=1333

Score = 206 bits (111), Expect = 1e-49
 Identities = 127/135 (95%), Gaps = 0/135 (0%)
 Strand=Plus/Plus

```

Query 339  TTTTGGGTGACAAAGTTTTCACCTTTTGAGAGCACTAAAAGAGCAGTACCTGAAATGTG 398
Sbjct 1034  TTTTAAAGTGACAAAGTTTTCACCTGTTGAGAGCACTAAAAGAGCTGTACCGAATAATGTG 1093

Query 399  GTCACCGGCTATGAAGAATGCATGGGGAGAGCTTATGATCAGTTGTTCAATGCAATCAA 458
Sbjct 1094  GTCACCGGCTATGAAGAATGCATGGGGAGAGCTTATGATCAGCTGTTGATGCCATTAA 1153

Query 459  ATCTGAAATGAAACC 473
Sbjct 1154  ATCTGAAATGAAACC 1168

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Sbjct 1073 AGTTC-GAAGTGAAACCTCC 1092

>gb|AF027215.1|AF027215 Trema orientalis hemoglobin gene, complete cds
Length=1101

Score = 158 bits (85), Expect = 4e-35
Identities = 123/141 (88%), Gaps = 3/141 (2%)
Strand=Plus/Plus

```
Query 339   TTTG-AGGTGACAAAGTTTGACATTTTGGAGACCATAAAAGAACGAGTACCTGAAATGT 397
           |||||
Sbjct 963   TTTGTAGGTCAACAAGTTTGACATTTTGGAGACCATAAAAGAACGAGTACCTGAAATGT 1012
Query 398   GGTCAACCGGCTATGAAGAATGCATGGGGAGAACCTTATGATCAGTTGGTCAATGCAATCA 457
           |||||
Sbjct 1013  GGTCAACCTGAGATGAAGAAGCATGGGGAGAACCTTATGATCAGTTGGTGGTCTGCTATCA 1072
Query 458   AAT-CTGAAATGAAACCTTCC 477
           |||||
Sbjct 1073  AGTTC-GAAGTGAAACCTCC 1092
```

>emb|AJ131351.1| Trema virgata gene encoding hemoglobin, isolate T4
Length=1104

Score = 145 bits (78), Expect = 3e-31
Identities = 120/140 (86%), Gaps = 3/140 (2%)
Strand=Plus/Plus

```
Query 340   TTTG-AGGTGACAAAGTTTGACATTTTGGAGACCATAAAAGAACGAGTACCTGAAATGTG 398
           |||||
Sbjct 957   TTTGTAGGTCAACAAGTTTGACATTTTGGAGACCATAAAAGAACGAGTACCTGAAATGTG 1016
Query 399   GTCACCGGCTATGAAGAATGCATGGGGAGAACCTTATGATCAGTTGGTCAATGCAATCAA 458
           |||||
Sbjct 1017  GTCAGCTGAGATGAAGAAGCATGGGGAGAACCTTATGATCAGTTGGTGGTCTGCTATCAA 1076
Query 459   AT-CTGAAATGAAACCTTCC 477
           |||||
Sbjct 1077  GTTC-GAAGTGAAACCTCC 1095
```

>emb|AJ131350.1| Trema virgata gene encoding hemoglobin, isolate T2
Length=1104

Score = 145 bits (78), Expect = 3e-31
Identities = 120/140 (86%), Gaps = 3/140 (2%)
Strand=Plus/Plus

```
Query 340   TTTG-AGGTGACAAAGTTTGACATTTTGGAGACCATAAAAGAACGAGTACCTGAAATGTG 398
           |||||
Sbjct 957   TTTGTAGGTCAACAAGTTTGACATTTTGGAGACCATAAAAGAACGAGTACCTGAAATGTG 1016
Query 399   GTCACCGGCTATGAAGAATGCATGGGGAGAACCTTATGATCAGTTGGTCAATGCAATCAA 458
           |||||
Sbjct 1017  GTCAGCTGAGATGAAGAAGCATGGGGAGAACCTTATGATCAGTTGGTGGTCTGCTATCAA 1076
Query 459   AT-CTGAAATGAAACCTTCC 477
           |||||
Sbjct 1077  GTTC-GAAGTGAAACCTCC 1095
```

>emb|AJ131349.1| Trema virgata gene encoding hemoglobin, isolate T1
Length=1103

Score = 145 bits (78), Expect = 3e-31
Identities = 120/140 (86%), Gaps = 3/140 (2%)
Strand=Plus/Plus

```
Query 340   TTTG-AGGTGACAAAGTTTGACATTTTGGAGACCATAAAAGAACGAGTACCTGAAATGTG 398
           |||||
Sbjct 956   TTTGTAGGTCAACAAGTTTGACATTTTGGAGACCATAAAAGAACGAGTACCTGAAATGTG 1015
Query 399   GTCACCGGCTATGAAGAATGCATGGGGAGAACCTTATGATCAGTTGGTCAATGCAATCAA 458
           |||||
Sbjct 1016  GTCAGCTGAGATGAAGAAGCATGGGGAGAACCTTATGATCAGTTGGTGGTCTGCTATCAA 1075
Query 459   AT-CTGAAATGAAACCTTCC 477
           |||||
Sbjct 1076  GTTC-GAAGTGAAACCTCC 1094
```